

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2001, 13:44:05 ; Search time 10.66 Seconds  
(without alignments)  
1693.494 Million cell updates/sec

Title: US-09-784-340-2

Sequence: 1 MSRSKALVFLLLQLPVCVC.....KCFLESCQKFNKTRKRE 527

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	7.6	527	1	UD16_RAT
2	33	6.3	528	1	UD14_RABIT
3	33	6.3	530	1	UD11_HUMAN
4	30	5.7	528	1	UD13_HUMAN
5	29	5.5	529	1	UD15_HUMAN
6	28	5.3	529	1	UD17_HUMAN
7	28	5.3	529	1	UD19_HUMAN
8	28	5.3	529	1	UD21_HUMAN
9	24	4.6	530	1	UD23_HUMAN
10	23	4.4	530	1	UD25_HUMAN
11	23	4.4	530	1	UD27_HUMAN
12	23	4.4	530	1	UD29_HUMAN
13	21	4.0	531	1	UD31_HUMAN
14	19	3.6	502	1	UD33_HUMAN
15	19	3.6	529	1	UD35_HUMAN
16	18	3.4	530	1	UD37_HUMAN
17	18	3.4	530	1	UD39_HUMAN
18	17	3.2	530	1	UD41_HUMAN
19	16	3.0	530	1	UD43_HUMAN
20	14	2.7	530	1	UD45_HUMAN
21	14	2.7	530	1	UD47_HUMAN
22	11	2.1	531	1	UD49_HUMAN
23	11	2.1	531	1	UD51_HUMAN
24	11	2.1	531	1	UD53_HUMAN
25	10	1.9	531	1	UD55_HUMAN
26	10	1.9	531	1	UD57_HUMAN
27	10	1.9	531	1	UD59_HUMAN
28	10	1.9	531	1	UD61_HUMAN
29	10	1.9	531	1	UD63_HUMAN
30	10	1.9	531	1	UD65_HUMAN
31	9	1.7	530	1	UD67_HUMAN
32	9	1.7	530	1	UD69_HUMAN
33	9	1.7	531	1	UD71_HUMAN

34	9	1.7	531	1	UD16_RABIT	028611 oryctolagus
35	9	1.7	532	1	UD14_RABIT	028612 oryctolagus
36	9	1.7	533	1	UD11_HUMAN	P22309 homo sapien
37	9	1.7	534	1	UD13_HUMAN	P35503 homo sapien
38	9	1.7	534	1	UD14_HUMAN	P22310 homo sapien
39	9	1.7	534	1	UD15_HUMAN	P35504 homo sapien
40	9	1.7	535	1	UD17_HUMAN	063886 mus musculu
41	8	1.5	98	1	PER_BUMPT	P13106 bumilleriop
42	8	1.5	515	1	HEMI_CLOVO	Q59292 clostridium
43	8	1.5	541	1	CGT_HUMAN	016880 homo sapien
44	8	1.5	541	1	CGT_MOUSE	064676 mus musculu
45	8	1.5	541	1	CGT_RAT	009426 rattus norv

## ALIGNMENTS

RESULT	ID	UD16_RAT	STANDARD	PRT	527 AA
AC	UD16_RAT	P36510			
DT	01-JUN-1994	(Rel. 29, Created)			
DT	01-JUN-1994	(Rel. 29, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	UDP-GLUCURONOSYLTRANSFERASE 2A1 PRECURSOR, MICROSOFT (EC 2.4.1.17)				
DE	(UDPRT) (UGT-OLP)				
GN	UGT2A1 OR UGT2A-1				
OS	Rattus norvegicus (Rat)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91156050; PubMed=1900353;				
RA	Lazard D., Zupko K., Porta Y., Nef P., Lazarevits J., Horn S.,				
RA	Khen M., Lancel D.;				
RT	"Odorant signal termination by olfactory UDP glucuronosyl				
RT	transferase";				
RL	Nature 349:790-793(1991).				
CC	-1- FUNCTION: UDPRT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND				
CC	SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND				
CC	ENDOGENOUS COMPOUNDS. THIS ISOFORM IS ACTIVE ON ODORANTS AND				
CC	SEEMS TO BE INVOLVED IN OLFACTION. IT COULD HELP CLEAR LIPOPHILIC				
CC	ODORANT MOLECULES FROM THE SENSORY EPITHELIUM.				
CC	-1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR				
CC	BETA-D-GLUCURONOSIDE.				
CC	-1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.				
CC	-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.				
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CC	-----				
DR	EMBL: X57565; NOT ANNOTATED. CDS.				
DR	InterPro: IPR002213; -				
DR	PFam: PF00201; UDPRT: 1.				
DR	PROSITE: PS00375; UDPRT: 1.				
KW	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;				
KW	MultiGene Family; Microsome; Olfaction.				
FT	SIGNAL	1	20	POTENTIAL.	
FT	CHAIN	21	527	UDP-GLUCURONOSYLTRANSFERASE 2A1.	
FT	TRANSMEM	491	507	POTENTIAL.	
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	313	313	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	527 AA;	59915 MW;	6A32A9B56EBE8B64;	

Query Match 7.6%; Score 40; DB 1; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3.8e-33;

Need  
NA search.

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 YKENAMRLSRHHDPVKPLDRAVFWIEFWVRHKGAKHLR 475  
 Db 436 YKENAMRLSRHHDPVKPLDRAVFWIEFWVRHKGAKHLR 475

RESULT 2  
 ID UDB4\_HUMAN STANDARD; PRT; 528 AA.  
 AC P06133; P36538; 060731; 060867;  
 DT 01-JAN-1998 (Rel. 06, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
 DE (UDPCT) (HYDROXYCHOLIC ACID) (HUC25) (UDPCH-1).  
 GN UGT2B4 OR UGT2B1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87241362; PubMed=3109396;  
 RA Jackson M.R., McCarthy L.R., Harding D., Wilson S., Coughtrie M.W.H.,  
 RA Burchell B.;  
 RT "Cloning of a human liver microsomal UDP-glucuronosyltransferase  
 RT cDNA.";  
 RL Biochem. J. 242:581-588(1987).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93326164; PubMed=8333863;  
 RA Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;  
 RT "cDNA cloning and expression of two new members of the human liver  
 RT UDP-glucuronosyltransferase 2B subfamily.";  
 RL Biochem. Biophys. Res. Commun. 194:436-503(1993).  
 RN (3)  
 RP SEQUENCE FROM N.A., AND VARIANT GLUT-458.  
 RA Levesque E., Beaulieu M., Belanger A.;  
 RT "UGT2B4(E458): a UDP-glucuronosyltransferase encoded by a polymorphic  
 RT gene with differential substrate specificity.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. ACTIVE ON POLYHYDROXYLATED ESTROGENS (SUCH  
 CC AS ESTRADIOL, 4-HYDROXYESTRONE AND 2-HYDROXYESTRADIOL) AND XENOBIOTICS  
 CC (SUCH AS 4-METHYLBELLIFERONE, 1-NAPHTHOL, 4-NITROPHENOL,  
 CC 2-AMINOPHENOL, 4-HYDROXYBIPHENYL, AND MENTHOL).  
 CC -1- FUNCTION: CAPABLE OF 6 ALPHA-HYDROXYGLUCURONIDATION OF  
 CC HYDROXYCHOLIC ACID.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -1- CAUTION: REF. 2 THOUGHT THAT THIS WAS A NEW FORM (UGT2B11). THE  
 CC NAME UGT2B11 HAS NOW BEEN REUSED FOR ANOTHER HUMAN ENZYME.  
 CC  
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 CC  
 CC EMBL: Y00317; CA68415.1; -;  
 CC EMBL: AF064200; AAC95002.1; -;  
 CC EMBL: AJ005162; CA60396.1; -;  
 CC PIR: A27878; A27878.  
 CC PIR: JN0619; JN0619.  
 CC MIM: 600067; -;

DR InterPro; IPR002213; -;  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferease; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome; Polymorphism.  
 FT SIGNAL 1 23  
 FT CHAIN 24 528  
 FT TRANSMEM 493 509  
 FT CARBOHYD 315 315  
 FT VARIANT 458 458  
 FT FT  
 FT CONFLICT 109 109  
 FT CONFLICT 171 172  
 FT CONFLICT 382 387  
 FT CONFLICT 396 396  
 SQ SEQUENCE 528 AA; 60512 MW; 6B45B6769971A078 CRC64;

Query Match 6.38; Score 33; DB 1; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-26;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 LSRHHDPVKPLDRAVFWIEFWVRHKGAKHLR 475  
 Db 445 LSRHHDPVKPLDRAVFWIEFWVRHKGAKHLR 477

RESULT 3  
 ID UDB4\_HUMAN STANDARD; PRT; 530 AA.  
 AC 075795;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B17 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
 DE (UDPCT) (C19-STERIOD SPECIFIC UDP-GLUCURONOSYLTRANSFERASE).  
 GN UGT2B17.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=96394358; PubMed=8798464;  
 RA Beaulieu M., Levesque E., Hum D.W., Belanger A.;  
 RT "Isolation and characterization of a novel cDNA encoding a human  
 RT UDP-glucuronosyltransferase active on C19 steroids.";  
 RL J. Biol. Chem. 271:22855-22862(1996).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98030207; PubMed=9364925;  
 RA Beaulieu M., Levesque E., Tchernof A., Beatty B.G., Belanger A.,  
 RA Hum D.W.;  
 RT "Chromosomal localization, structure, and regulation of the UGT2B17  
 RT gene, encoding a C19 steroid metabolizing enzyme.";  
 RL DNA Cell Biol. 16:1143-1154(1997).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. THE MAJOR SUBSTRATES OF THIS ISOZYME ARE  
 CC ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >  
 CC ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >  
 CC ANDROSTANE-3ALPHA,17BETA-DIOL (3ALPHA-DIOL) > TESTOSTERONE >  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES INCLUDING THE  
 CC LIVER, KIDNEY, TESTIS, UTERUS, PLACENTA, MAMMARY GLAND, ADRENAL  
 CC GLAND, SKIN, AND PROSTATE.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U59209; AAC25491.1; -  
DR MIM: 601903; -  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KM Multigene family; Microsome.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 1 530 UDP-GLUCURONOSYLTRANSFERASE 2B17.  
FT TRANSMEM 495 515 POTENTIAL.  
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 530 AA; 61095 MW; 8E59EBC43CF43760 CRC64;  
  
Query Match 6.3%; Score 33; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 6.5e-26;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 443 LSRHHDPYKPLDRAVFWIEFWMRHKGAKHLR 475  
DB 446 LSRHHDPYKPLDRAVFWIEFWMRHKGAKHLR 478  
|||||  
  
RESULT 4  
ID UDB1\_MACFA STANDARD; PRT; 528 AA.  
AC 09XN55;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B19 PRECURSOR, MICROSOMAL (EC 2.4.1.17).  
GN UGT2B19.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver, and Prostate;  
RX MEDLINE=99203465; PubMed=10102998;  
RA Belanger G., Barbier O., Hum D.W., Belanger A.;  
RT "Molecular cloning, expression and characterization of a monkey  
RT steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates  
RT testosterone";  
RN Eur. J. Biochem. 260:701-708(1999).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD  
CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES: EUGENOL, 4-  
CC METHYLBELMELIFERONE, P-NITROPHENOL, 1-NAPHTHOL, P,P'-BIPHENOL,  
CC NARINGENIN AND O,O'-BIPHENOL. ACTIVE ALSO ON 3A-HYDROXY AND 17B-  
CC HYDROXY POSITIONS OF STEROIDS.  
CC -1- FUNCTION: CONTRIBUTES TO THE FORMATION OF ANDROGEN GLUCURONIDE IN  
CC EXTRAHEPATIC STEROID TARGET TISSUES SUCH AS THE PROSTATE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, OVARY, PROSTATE, COLON,  
CC KIDNEY, PANCREAS, BRAIN, CEREBELLUM, MAMMARY GLAND AND EPIDIDYMS.  
CC NOT EXPRESSED IN SMALL INTESTINE, SPLEEN, BLADDER, ADRENAL GLAND  
CC AND TESTIS.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
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CC -----  
DR EMBL: AF112112; MAD24435.1; -  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KM Multigene family; Microsome.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 1 528 UDP-GLUCURONOSYLTRANSFERASE 2B19.  
FT TRANSMEM 493 513 POTENTIAL.  
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 528 AA; 60741 MW; 3BFD2AE714A27AE CRC64;  
  
Query Match 5.7%; Score 30; DB 1; Length 528;  
Best Local Similarity 100.0%; Pred. No. 8.2e-23;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 446 IHHDQPYKPLDRAVFWIEFWMRHKGAKHLR 475  
DB 448 IHHDQPYKPLDRAVFWIEFWMRHKGAKHLR 477  
|||||  
  
RESULT 5  
ID UDB1\_RAT STANDARD; PRT; 529 AA.  
AC P09875;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-JUN-1999 (Rel. 38, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPGT) (UDPGTR-2).  
GN UGT2B1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86196018; PubMed=3084479;  
RA McKenzie P.I.;  
RT "rat liver UDP-glucuronosyltransferase. Sequence and expression of a  
RT cDNA encoding a phenobarbital-inducible form";  
RN J. Biol. Chem. 261:6119-6125(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90293083; PubMed=2113533;  
RA McKenzie P.I., Rodboun L.;  
RT "Organization of the rat UDP-glucuronosyltransferase, UDPGTR-2, gene  
RT and characterization of its promoter";  
RN J. Biol. Chem. 265:11328-11332(1990).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- INDUCTION: BY PHENOBARBITAL.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY  
CC -----  
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CC EMBL: M13506; AAA42313.1; -  
 DR EMBL: M35086; AAA42310.1; -  
 DR EMBL: M35202; AAA42310.1; JOINED.  
 DR EMBL: M35080; AAA42310.1; JOINED.  
 DR EMBL: M35082; AAA42310.1; JOINED.  
 DR EMBL: M35083; AAA42310.1; JOINED.  
 DR PIR: A24324; A24324.  
 DR PIR: A24233; A24233.  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT.1  
 DR PROSITE: PS00375; UDPGT.1  
 KM Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KM Multigene family; Microsome.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 529 UDP-GLUCURONOSYLTANSFERASE 2B1.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 529 AA: 60484 MW: 14DF0224BF1C3044 CRC64;

Query Match 5.5%; Score 29; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-22;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 435 SYKENAMRLSRHHDPKPLDRAVFWIE 463  
 Db 438 SYKENAMRLSRHHDPKPLDRAVFWIE 466

RESULT 6  
 ID UDBA HUMAN STANDARD; PRT; 528 AA.  
 AC P36537;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTANSFERASE 2B10 PRECURSOR, MICROSMAL (EC 2.4.1.17) (UDPGT).  
 GN UGT2B10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=93326164; PubMed=8333863;  
 RT Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;  
 RT "cDNA cloning and expression of two new members of the human liver  
 RT UDP-glucuronosyltransferase 2B subfamily";  
 RT Biochem. Biophys. Res. Commun. 194:496-503(1993).  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCONOSIDE.  
 CC -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTANSFERASE FAMILY.

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DR EMBL: X63359; CAA44961.1; -  
 DR PIR: JN0620; JN0620.  
 DR MIM: 600070; -

DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT.1  
 DR PROSITE: PS00375; UDPGT.1  
 KM Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KM Multigene family; Microsome.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 528 UDP-GLUCURONOSYLTANSFERASE 2B10.  
 FT TRANSMEM 492 512 POTENTIAL.  
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 528 AA: 60774 MW: 5E6EA3DC032C2E0 CRC64;

Query Match 5.3%; Score 28; DB 1; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-21;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 448 HDQPKPLDRAVFWIEFVHRHGAHLR 475  
 Db 449 HDQPKPLDRAVFWIEFVHRHGAHLR 476

RESULT 7  
 ID UDB7 HUMAN STANDARD; PRT; 529 AA.  
 AC P16662;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTANSFERASE 2B7 PRECURSOR, MICROSMAL (EC 2.4.1.17) (UDPGT) (3,4-CATECHOL ESTROGEN SPECIFIC) (UDPETH-2).  
 GN UGT2B7 OR UGT2B9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=90243659; PubMed=2159463;  
 RT Ritter J.K., Sheen Y.Y., Owens I.S.;  
 RT "Cloning and expression of human liver UDP-glucuronosyltransferase in  
 RT COS-1 cells. 3,4-catechol estrogens and estril as primary  
 RT substrates";  
 RT J. Biol. Chem. 265:7900-7906(1990).  
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -!- FUNCTION: ITS UNIQUE SPECIFICITY FOR 3,4-CATECHOL ESTROGENS AND  
 CC ESTRIOL SUGGESTS IT MAY PLAY AN IMPORTANT ROLE IN REGULATING THE  
 CC LEVEL AND ACTIVITY OF THESE POTENT AND ACTIVE ESTROGEN  
 CC METABOLITES.  
 CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCONOSIDE.  
 CC -!- SUBCELLULAR LOCATION: MICROSMAL.  
 CC -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTANSFERASE FAMILY.

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DR EMBL: J05428; AAA36793.1; -  
 DR PIR: A35366; A35366.  
 DR MIM: 600068; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPGT.1  
 DR PROSITE: PS00375; UDPGT.1  
 KM Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;

Query Match 5.3%; Score 28; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.5e-21;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

448 HDQPVKPLDRAVWIEFVNRHGAKHLR 475  
450 HDQPVKPLDRAVWIEFVNRHGAKHLR 477

RESULT 8  
DDB9\_MACFA STANDARD; PRT; 529 AA.  
AC 002663;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B9 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPCT).  
GN UGT2B9.  
OS Maccaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Maccaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=98030212; PubMed=9364930;  
RA Belanger G., Beaulieu M., Levesque E., Hum D.W., Belanger A.;  
RT "Expression and characterization of a novel  
UDP-glucuronosyltransferase, UGT2B9, from cynomolgus monkey.";  
RT DNA Cell Biol. 16:1195-1205(1997).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
ENDOGENOUS COMPOUNDS. THIS ISOZYME IS ACTIVE ON C18, C19, AND C21  
STEROIDS, BILE ACIDS, AND SEVERAL XENOBIOTICS INCLUDING EUGENOL,  
1-NAPHTHOL, AND P-NITROPHENOL.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: U91582; AAB50249.1; -  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT SIGNAL 1  
FT CHAIN 1  
FT TRANSMEM 494 514  
FT CARBOHYD 67 67  
FT CARBOHYD 68 68  
FT CARBOHYD 88 88  
SQ SEQUENCE 529 AA: 60970 MW; F110F85FE3A9B8D CRC64;

Query Match 5.3%; Score 28; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 9.5e-21;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

448 HDQPVKPLDRAVWIEFVNRHGAKHLR 475  
450 HDQPVKPLDRAVWIEFVNRHGAKHLR 477

RESULT 9  
UDBC\_RAT STANDARD; PRT; 530 AA.  
AC P36511;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B12 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPCT).  
GN UGT2B12.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver, and Kidney;  
RX MEDLINE=96032669; PubMed=7574722;  
RA Green M.D., Clarke D.J., Oturu E.M., Styczynski P.B.,  
RA Jackson M.R., Burchell B., Tephly T.R.;  
RT "Cloning and expression of a rat liver phenobarbital-inducible UDP-  
glucuronosyltransferase (2B12) with specificity for monoterpenoid  
alcohols.";  
RT Arch. Biochem. Biophys. 322:460-468(1995).  
RN [2]  
RP SEQUENCE OF 24-38. AND CHARACTERIZATION.  
RC STRAIN=MISTAR; TISSUE=Liver;  
RX MEDLINE=9131237; PubMed=1906977;  
RA Styczynski P.B., Green M.S., Pulg J., Coffman B.L., Tephly T.R.;  
RT "Purification and properties of a rat liver phenobarbital-inducible  
4-hydroxybiphenyl UDP-glucuronosyltransferase.";  
RT Mol. Pharmacol. 40:80-84(1991).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
ENDOGENOUS COMPOUNDS. CATALYZES THE TRANSFER OF GLUCURONIC ACID  
FROM UDP-GLUCURONIC ACID TO VARIOUS AGLYCON MOLECULES. CATALYZES  
THE GLUCURONIDATION OF MONOTERPENOID ALCOHOLS, SUCH AS (-)-  
BORNEOL, (+)-MENTHOL, AND (-)-NOROL. IN ADDITION, A NUMBER OF  
SIMPLE PHENOLIC COMPOUNDS, SUCH AS HYDROXYBIPHENYLS, 7-  
HYDROXYLATED COUMARINS, P-NITROPHENOL, AND FOOD-DERIVED SUBSTANCES  
(E.G., NARINGENIN AND EUGENOL), AND 4-METHYLBELBILIFERONE ARE ALSO  
SUBSTRATES.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS SEEN IN THE KIDNEY AND  
TESTIS.  
CC -1- INDUCTION: BY PHENOBARBITAL.  
CC -1- PTM: N-GLYCOSYLATED (PROBABLE).  
CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE LIVER ISOZYME.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: U06273; AAB3404.1; -

DR EMBL: U06274; AAA83405.1; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPCT: 1.  
 DR PROSITE: PS00375; UDPCT: 1.  
 KM Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 23  
 FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B12.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC.. ) (POTENTIAL).  
 FT VARIANT 2 2 S -> P (IN KIDNEY).  
 FT VARIANT 61 61 F -> S (IN KIDNEY).  
 FT VARIANT 71 71 D -> H (IN KIDNEY).  
 FT VARIANT 95 95 N -> S (IN KIDNEY).  
 FT VARIANT 183 183 Q -> K (IN KIDNEY).  
 FT VARIANT 346 346 P -> T (IN KIDNEY).  
 FT VARIANT 398 398 A -> G (IN KIDNEY).  
 FT VARIANT 414 415 VE -> AT (IN KIDNEY).  
 FT VARIANT 433 433 V -> D (IN KIDNEY).  
 FT VARIANT 475 475 K -> L (IN KIDNEY).  
 FT VARIANT 488 488 Q -> L (IN KIDNEY).  
 SQ SEQUENCE 530 AA; 61060 MW; D49313CE3ED5BFD CRC64;

Query Match 4.6%; Score 24; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 453 KPLDRAVWIEFWYMRHKGAKHLR 476  
 DB 456 KPLDRAVWIEFWYMRHKGAKHLR 479  
 |||||||

## RESULT 10

UDP8\_RAT STANDARD; PRT; 530 AA.  
 ID UDP8\_RAT  
 AC 062789;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B8 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UGT2B-RH4).  
 GN UGT2B8.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H12G-;  
 RA Cohen H., Trus M., Benvenisty N., Reshef L.;  
 RT "A novel member of the UDPCT family is abundantly expressed in  
 RT H4IIEG3 hepatoma cells.";  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U27518; AAA86833.1; -  
 DR InterPro: IPR002213; -  
 DR Pfam: PF00201; UDPCT: 1.

DR PROSITE: PS00375; UDPCT; FALSE\_NEG.  
 KM Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 530 UDP-GLUCURONOSYLTRANSFERASE 2B8.  
 FT TRANSMEM 496 516 POTENTIAL.  
 FT CARBOHYD 316 316 N-LINKED (GLCNAC.. ) (POTENTIAL).  
 SQ SEQUENCE 530 AA; 60089 MW; 53251950C6CAEDE CRC64;

Query Match 4.4%; Score 23; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-15;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 453 KPLDRAVWIEFWYMRHKGAKHLR 475  
 DB 457 KPLDRAVWIEFWYMRHKGAKHLR 479  
 |||||||

## RESULT 11

UDP8\_HUMAN STANDARD; PRT; 530 AA.  
 ID UDP8\_HUMAN  
 AC P54855; P23765; Q9UK63;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B15 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UDPCTH-3) (HUG4).  
 GN UGT2B15 OR UGT2B8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RC MEDLINE=95136867; PubMed=7835232;  
 RA Green M.D., Oclun E.M., Teply T.R.;  
 RT "Stable expression of a human liver UDP-glucuronosyltransferase  
 RT (UGT2B15) with activity toward steroid and xenobiotic substrates.";  
 RL Drug Metab. Dispos. 22:79-805(1994).  
 RN [2]  
 RP SEQUENCE OF 8-530 FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RC MEDLINE=9034358; PubMed=2116769;  
 RA Coffman B.L., Teply T.R., Irshaid Y.M., Green M.D., Smith C.,  
 RA Jackson M.R., Wooster R., Burchell B.;  
 RT "Characterization and primary sequence of a human hepatic microsomal  
 RT estril UDP-glucuronosyltransferase.";  
 RL Arch. Biochem. Biophys. 281:170-175(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT TYR-85.  
 RX MEDLINE=97439504; PubMed=9295060;  
 RA Levesque E., Beaulieu M., Green M.D., Teply T.R., Belanger A.,  
 RA Hum D.W.;  
 RT "Isolation and characterization of UGT2B15(Y85): a  
 RT UDP-glucuronosyltransferase encoded by a polymorphic gene.";  
 RL Pharmacogenetics 7:317-325(1997)  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD  
 CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES, INCLUDING SIMPLE  
 CC PHENOLIC COMPOUNDS, 7-HYDROXYLATED COMARINS, FLAVONOIDS,  
 CC ANTHRAQUINONES, AND CERTAIN DRUGS AND THEIR HYDROXYLATED  
 CC METABOLITES. IT ALSO CATALYZES THE GLUCURONIDATION OF ENDOGENOUS  
 CC ESTROGENS AND ANDROGENS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC CAUTION: REF.2 THOUGHT THAT THIS WAS A SEPARATE FORM (UGT2B8). THE  
 CC NAME UGT2B8 HAS NOW BEEN REUSED FOR A RAT ENZYME.

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DR EMBL; U08854; AAC50077.1; -  
DR EMBL; U06641; AAA83406.1; -  
DR EMBL; AF180332; AAD55093.1; -  
DR PIR; S11309; S11309.  
DR MIM; 600069; -  
DR InterPro; IPR002213; -  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Polymorphism.  
FT SIGNAL 1 23  
FT CHAIN 1 23  
FT TRANSMEM 24 530  
FT CARBOHYD 495 515  
FT CARBOHYD 316 316  
FT CARBOHYD 483 483  
FT VARIANT 85 85  
FT CONFLICT 119 119  
FT CONFLICT 145 145  
FT CONFLICT 150 155  
FT CONFLICT 162 162  
FT CONFLICT 165 165  
FT CONFLICT 170 177  
FT CONFLICT 181 181  
FT CONFLICT 203 203  
FT CONFLICT 293 293  
FT CONFLICT 401 401  
FT CONFLICT 443 443  
FT CONFLICT 501 501  
FT CONFLICT 523 523  
SQ SEQUENCE 530 AA; 60961 MW; 23DDA4B9687ECBA CRC64;

Query Match 4.4%; Score 23; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 1.4e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 KPLDRAVFWIEFVNRHKGAKHLR 475  
Db 456 KPLDRAVFWIEFVNRHKGAKHLR 478

RESULT 12  
UDBD\_MACFA STANDARD; PRT; 530 AA.  
AC 077649;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B20 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UNPRT).  
GN UGT2B20.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OC NCBI\_Taxid=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver, and Prostate;  
RA Barbier O., Belanger A., Hum D.W.;  
RT "Cloning and characterization of a simian UDP-glucuronosyltransferase  
enzyme, UGT2B20, a novel steroid conjugating protein.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC  
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DR EMBL; AF072223; AAD08808.1; -  
DR InterPro; IPR002213; -  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT SIGNAL 1 23  
FT CHAIN 1 23  
FT TRANSMEM 24 530  
FT CARBOHYD 495 515  
FT CARBOHYD 65 65  
FT CARBOHYD 103 103  
FT CARBOHYD 316 316  
FT CARBOHYD 483 483  
SQ SEQUENCE 530 AA; 61225 MW; A5EB47F8D517D8DA CRC64;

Query Match 4.4%; Score 23; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 1.4e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 KPLDRAVFWIEFVNRHKGAKHLR 475  
Db 456 KPLDRAVFWIEFVNRHKGAKHLR 478

RESULT 13  
UDBD\_RABIT STANDARD; PRT; 531 AA.  
AC P36512;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UNPRT) (EC10).  
GN UGT2B13.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OC NCBI\_Taxid=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;  
RX MEDLINE=93315511; PubMed=8325897;  
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green N.D., Teply T.R.;  
RT "Cloning and characterization of rabbit liver UDP-  
RT glucuronosyltransferase cDNAs. Developmental and inducible expression  
RT of 4-hydroxybiphenyl UGT2B13.";  
RL J. Biol. Chem. 268:15260-15266(1993).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENOGENOUS COMPOUNDS. ACTS ON SMALL PHENOLIC AGENTS SUCH AS 2-  
CC NAPHTHOL AND 4-METHYLBELLIFERONE AS WELL AS BULKY PHENOLIC  
CC COMPOUNDS LIKE 2-HYDROXY- AND 4-HYDROXYBIPHENYL. IN CONTRAST TO  
CC 2B16 IT IS ACTIVE TOWARD OCTYLGALATE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.

```

CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBIT.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
CC EMBL: L01083; AAA18020.1; -
CC PIR: B47113; B47113.
CC InterPro: IPR002213; -
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC Multigene family; Microsome.
CC SIGNAL
CC CHAIN 1 24 UDP-GLUCURONOSYLTRANSFERASE 2B13.
CC TRANSMEM 25 531 POTENTIAL.
CC CARBOHYD 495 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 531 AA; 60552 MW; 961DA58AC4CB9932 CRC64;

Query Match 4.0%; Score 21; DB 1; Length 531;
Best Local Similarity 100.0%; Pred. No. 1,6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 354 WIPONDILGHFKTKAFITHG 374
Db 358 WIPONDILGHFKTKAFITHG 378

RESULT 14
UDCL_RABBIT STANDARD: PRT; 502 AA.
AC P36514;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE (FRAGMENT).
GN UGT2C1 OR UGT2A2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
RX MEDLINE=93315511; Pubmed=8325897;
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
RT "Cloning and characterization of rabbit liver UDP-
RT glucuronosyltransferase cDNAs. Developmental and inducible expression
RT of 4-hydroxydiphenyl UGT2B13."
RL J. Biol. Chem. 268:15260-15266(1993).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
CC EMBL: L01083; AAA18023.1; -
CC PIR: B47113; B47113.
CC InterPro: IPR002213; -
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferase: Glycosyltransferase; Glycoprotein; Transmembrane;
CC Multigene family; Microsome.
CC SIGNAL
CC CHAIN 1 177 POTENTIAL.
CC TRANSMEM 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 502 AA; 57449 MW; B5B565670BFAE1D35 CRC64;

Query Match 3.6%; Score 19; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 1,8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPLDRAVFIWIEVRRKGA 471
Db 428 KPLDRAVFIWIEVRRKGA 446

RESULT 15
UDBR_HUMAN STANDARD: PRT; 529 AA.
AC O75310;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B11 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT).
GN UGT2B11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98340847; Pubmed=9675083;
RA Beaulieu M., Levesque E., Hum D.W., Belanger A.;
RT "Isolation and characterization of a human orphan UDP-
RT glucuronosyltransferase, UGT2B11."
RL Biochem. Biophys. Res. Commun. 248:44-50(1998).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
CC EMBL: AF016492; AAC27891.1; -
CC MIM: 603064; -
CC InterPro: IPR002213; -
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
CC Multigene family; Microsome.
CC SIGNAL
CC CHAIN 1 21 POTENTIAL.
CC TRANSMEM 22 529 UDP-GLUCURONOSYLTRANSFERASE 2B11.

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FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 529 AA; 61038 MW; CEACAC3C71CFC2AB4 CRC64;

Query Match 3.6%; Score 19; DB 1; Length 529;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 448 HDQPVKPLDRAVWIEFVM 466  
DB 450 HDQPVKPLDRAVWIEFVM 468

## RESULT 16

UDB3\_RAT STANDARD; PRT; 530 AA.  
ID UDB3\_RAT P08542; P16915;  
AC 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1990 (Rel. 15, Last annotation update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B3 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (TESTOSTERONE, DIHYDROTESTOSTERONE, AND BETA-ESTRADIOL SPECIFIC) (17-BETA-HYDROXYSTEROID SPECIFIC) (UDPCTR-3) (RUG38).  
GN UGT2B3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=87250645; PubMed=3110162;  
RA McKenzie P.I.;  
RT \*Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two enzymes which glucuronidate testosterone, dihydrotestosterone, and beta-estradiol.  
RT J. Biol. Chem. 262:9744-9749(1987).  
RL [2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=87231096; PubMed=3108864;  
RA Harding D., Wilson S.M., Jackson M.R., Burchell B., Green M.D., Teply T.R.;  
RT \*Nucleotide and deduced amino acid sequence of rat liver 17 beta-hydroxysteroid UDP-glucuronosyltransferase.  
RT Nucleic Acids Res. 15:3936-3936(1987).  
RL [3]  
RN [3]  
RP FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS. 2B3 IS ACTIVE ON TESTOSTERONE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC -1- BETA-D-GLUCORONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- INDUCTION: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
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CC -----  
CC EMBL: M3109; AAA41280.1; -  
CC EMBL: Y00156; CAA6351.1; -  
CC PIR: A28460; A28460.  
CC PIR: S07390; S07390.  
CC InterPro: IPR002213; -  
CC Pfam: PF00201; UDPCT; 1.  
CC PROSITE: PS00375; UDPCT; 1.  
CC Transfaser: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KM Multigene family; Microsome.  
FT SIGNAL 1 23 BY SIMILARITY.

FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B3.  
FT TRANSMEM 494 510 POTENTIAL.  
FT CONFLICT 54 54 T -> S (IN CAA68351).  
FT CONFLICT 119 119 G -> E (IN REF. 2).  
FT CONFLICT 376 376 S -> G (IN REF. 2).  
FT CONFLICT 424 424 S -> T (IN REF. 2).  
FT CONFLICT 500 500 T -> S (IN REF. 2).  
SQ SEQUENCE 530 AA; 60524 MW; BB633D70DBE8A7E4 CRC64;

Query Match 3.4%; Score 18; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 AVFWIEFMRHKGAKHLR 475  
DB 461 AVFWIEFMRHKGAKHLR 478

## RESULT 17

UDBE\_RABIT STANDARD; PRT; 530 AA.  
ID UDBE\_RABIT P36513;  
AC 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B14 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (EGT12).  
GN UGT2B14.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;  
RX MEDLINE=93315511; PubMed=8325897;  
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Teply T.R.;  
RT \*Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.  
RT J. Biol. Chem. 268:15260-15266(1993).  
RL [4]  
RN [4]  
RP FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC -1- BETA-D-GLUCORONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC -----  
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CC -----  
CC EMBL: L01082; AAA18021.1; -  
CC PIR: CA7113; CA7113.  
CC InterPro: IPR002213; -  
CC Pfam: PF00201; UDPCT; 1.  
CC PROSITE: PS00375; UDPCT; 1.  
CC Transfaser: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KM Multigene family; Microsome.  
FT SIGNAL 1 24 BY SIMILARITY.  
FT CHAIN 25 530 UDP-GLUCURONOSYLTRANSFERASE 2B14.  
FT TRANSMEM 494 510 POTENTIAL.  
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 530 AA; 60664 MW; CEAA4BF25B53CB35 CRC64;

Query Match 3.4%; Score 18; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2, 1e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 YDMTPONDLLGHPRKTKAF 369  
 DB 355 YDMTPONDLLGHPRKTKAF 372

RESULT 18  
 UDB5\_MOUSE STANDARD; PRT; 530 AA.  
 ID UDB5\_MOUSE  
 AC P17717;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B5 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 GN UGT2B5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6N; TISSUE=Liver;  
 RX MEDLINE=88029469; PubMed=3117546;  
 RA Kimura T., Owens I.S.;  
 RT Mouse UDP glucuronosyltransferase. cDNA and complete amino acid  
 sequence and regulation.";  
 RL Eur. J. Biochem. 168:515-521(1987).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
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 CC -----  
 DR EMBL; X06358; CAA29657.1; -;  
 DR PIR; S00163; S00163.  
 DR MGD; MGI:98900; Ugt2b5.  
 DR InterPro: IPR002213; -;  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT SIGNAL 1 23  
 FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B5.  
 FT TRANSMEM 494 510 POTENTIAL.  
 FT CARBOHYD 316 316 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 530 AA; 60856 MW; 7BAFEE9EFA866B3 CRC64;

Query Match 3.2%; Score 17; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 2, 2e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPLDRAVWIEFVVRHK 469  
 DB 456 KPLDRAVWIEFVVRHK 472

RESULT 19  
 UDB6\_RABIT STANDARD; PRT; 523 AA.  
 ID UDB6\_RABIT  
 AC O19103;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B16 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 GN UGT2B16.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=97166166; PubMed=9013565;  
 RA Li O., Lou X., Peyronneau M.-A., Straub P.O., Tukey R.H.;  
 RT Expression and functional domains of rabbit liver UDP-  
 glucuronosyltransferase 2B16 and 2B13.";  
 RL J. Biol. Chem. 272:3272-3279(1997).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS. ACTS ON SMALL PHENOLIC AGENTS SUCH AS 2-  
 NAPHTHOL AND 4-METHYLBELLIFERONE AS WELL AS BULKY PHENOLIC  
 COMPOUNDS LIKE 2-HYDROXY- AND 4-HYDROXYBIPHENYL. IN CONTRAST TO  
 2B13 IT IS ACTIVE TOWARD 4-HYDROXYESTERONE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
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 CC -----  
 DR EMBL; U72742; AAB71494.1; -;  
 DR InterPro: IPR002213; -;  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT NON\_TER 1 1  
 FT SIGNAL 1 16  
 FT CHAIN 17 523 UDP-GLUCURONOSYLTRANSFERASE 2B16.  
 FT TRANSMEM 487 503 POTENTIAL.  
 FT CARBOHYD 309 309 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 523 AA; 60077 MW; 224088E768ED3DE CRC64;

Query Match 3.0%; Score 16; DB 1; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 2, 4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 460 FWIEFVVRHKGAKHR 475  
 DB 456 FWIEFVVRHKGAKHR 471

RESULT 20  
 UDB2\_RAT STANDARD; PRT; 530 AA.  
 ID UDB2\_RAT  
 AC P08541;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 2B2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 GN UGT2B2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=97166166; PubMed=9013565;  
 RA Li O., Lou X., Peyronneau M.-A., Straub P.O., Tukey R.H.;  
 RT Expression and functional domains of rabbit liver UDP-  
 glucuronosyltransferase 2B16 and 2B13.";  
 RL J. Biol. Chem. 272:3272-3279(1997).  
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDOGENOUS COMPOUNDS. ACTS ON SMALL PHENOLIC AGENTS SUCH AS 2-  
 NAPHTHOL AND 4-METHYLBELLIFERONE AS WELL AS BULKY PHENOLIC  
 COMPOUNDS LIKE 2-HYDROXY- AND 4-HYDROXYBIPHENYL. IN CONTRAST TO  
 2B13 IT IS ACTIVE TOWARD 4-HYDROXYESTERONE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY IN ADULT RABBITS.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC  
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 CC -----  
 DR EMBL; U72742; AAB71494.1; -;  
 DR InterPro: IPR002213; -;  
 DR Pfam; PF00201; UDPGT; 1.  
 DR PROSITE; PS00375; UDPGT; 1.  
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 KW Multigene family; Microsome.  
 FT NON\_TER 1 1  
 FT SIGNAL 1 16  
 FT CHAIN 17 523 UDP-GLUCURONOSYLTRANSFERASE 2B16.  
 FT TRANSMEM 487 503 POTENTIAL.  
 FT CARBOHYD 309 309 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 523 AA; 60077 MW; 224088E768ED3DE CRC64;

GN UGT2B2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=87033594; PubMed=2429951;  
RA McKenzie P.I.;  
RT "Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression  
of a form glucuronidating 3-hydroxyandrogens.";  
RT J. Biol. Chem. 261:14112-14117(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91369480; PubMed=1909872;  
RA Haque S.J., Peterson D.D., Nebert D.W., McKenzie P.I.;  
RT "Isolation, sequence, and developmental expression of rat UGT2B2: the  
gene encoding a constitutive UDP glucuronosyltransferase that  
metabolizes etiocholanolone and androstereone.";  
RT DNA Cell Biol. 10:515-524(1991).  
RN [3]  
RP SEQUENCE OF 30-530 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86120371; PubMed=3003696;  
RA Jackson M.R., Burchell B.;  
RT "The full length coding sequence of rat liver androstereone UDP-  
glucuronyltransferase cDNA and comparison with other members of this  
gene family.";  
RT Nucleic Acids Res. 14:779-795(1986).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
ENDOGENOUS COMPOUNDS. 2B2 ACTS ON VARIOUS ENDOGENOUS STEROIDS,  
ESPECIALLY ETIOCHOLANOLONE AND ANDROSTERONE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- INDUCTION: CONSTITUTIVELY EXPRESSED.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: J02589; AAA42314.1; -  
DR EMBL: M74459; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: X03478; CAA27198.1; -  
DR PIR: A26064; A26064.  
DR PIR: A23520; A23520.  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT. 1.  
DR PROSITE: PS00375; UDPGT. 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT CHAIN 1 23  
FT SIGNAL 1 23  
FT TRANSMEM 24 530  
FT CARBOHYD 316 510  
FT CONFLICT 159 159 D -> E (IN REF. 3).  
FT CONFLICT 286 286 A -> S (IN REF. 3).  
FT CONFLICT 351 351 N -> I (IN REF. 3).  
FT CONFLICT 363 363 L -> I (IN REF. 3).  
FT CONFLICT 363 363  
SQ SEQUENCE 530 AA; 60985 MW; F2FFFE23E2D75B2 CRC64;

Query Match 2.7%; Score 14; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPTKAF 369  
ID |||||||||||||  
Db 359 PONDLLGHPTKAF 372  
RESULT 21  
ID UDB6\_RAT STANDARD; PRT; 530 AA.  
AC P19468;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 2B6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPGT) (17-BETA-HYDROXYSTEROID SPECIFIC) (UDPGT-5).  
GN UGT2B6.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90256795; PubMed=1692835;  
RA McKenzie P.I.;  
RT "The cDNA sequence and expression of a variant 17 beta-hydroxysteroid  
UDP-glucuronosyltransferase.";  
RT J. Biol. Chem. 265:8699-8703(1990).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
ENDOGENOUS COMPOUNDS. 2B6 IS ABOUT 30-FOLD LESS ACTIVE THAN 2B3  
TOWARD TESTOSTERONE AND DIHYDROTESTOSTERONE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- INDUCTION: CONSTITUTIVELY EXPRESSED.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
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CC -----  
DR EMBL: M33746; AAA03216.1; -  
DR EMBL: M33746; AAA03217.1; -  
DR PIR: A36276; A36276.  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT. 1.  
DR PROSITE: PS00375; UDPGT. 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome.  
FT CHAIN 1 23  
FT SIGNAL 1 23  
FT TRANSMEM 494 510  
FT TRANSMEM 494 510  
SQ SEQUENCE 530 AA; 60593 MW; F6B23E3469BDBDEA CRC64;

Query Match 2.7%; Score 14; DB 1; Length 530;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPTKAF 369  
ID |||||||||||||  
Db 359 PONDLLGHPTKAF 372  
RESULT 22  
ID UDB6\_MOUSE STANDARD; PRT; 531 AA.  
AC 064435; 062580; P70692;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UGT1\*6) (UGT1-06) (UGT1.6) (UGT1A6) (UGT1A1) (PHENOL UDP-  
 GN GLUCURONOSYLTRANSFERASE).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/CBA; TISSUE=Liver;  
 RA Reuter S.F., Vasilou V., Puga A., Nebert D.W.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.  
 RC STRAIN=C57BL/6; TISSUE=Liver;  
 RX MEDLINE=94347791; PubMed=8068691;  
 RA Lamb J.G., Straub P., Tukey R.H.;  
 RT "Cloning and characterization of cDNAs encoding mouse Ugt1.6 and  
 RT rabbit UGT1.6: differential induction by  
 RT 2,3,7,8-tetrachlorodibenzo-p-dioxin";  
 RL Biochemistry 33:10513-10520(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=95408245; PubMed=7677729;  
 RA Koike O., Hasada K., Yasui Y., Sakai Y., Sato H., Watanabe T.;  
 RT "Isolation of cDNAs for mouse phenol and bilirubin UDP-  
 RT glucuronosyltransferase (Ugt1a) to chromosome 1 by restriction  
 RT fragment length variations";  
 RL Biochem. Genet. 33:111-122(1995).  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. CONJUGATES SMALL PLANAR PHENOLIC MOLECULES  
 CC SUCH AS 4-NITROPHENOL, 1-NAPHTHOL, AND 4-METHYLBELLIFERONE. THE  
 CC BULKY PHENOL 4-HYDROXYBIPHENYL, ANDROGENS AND ESTROGENS ARE NOT  
 CC SUBSTRATES. 2-HYDROXYBIPHENYL IS AN EXCELLENT SUBSTRATE.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- INUNCTION: BY DIOXIN.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U16818; AAA65979.1; -  
 CC EMBL: U09930; AAA51871.1; -  
 CC EMBL: D87867; BAA13483.1; -  
 CC MGD: MGI:98898; Ugt1a1.  
 CC InterPro: IPR002213; -  
 CC Pfam: PF00201; UDPCT; 1.  
 CC PROSITE: PS00375; UDPCT; 1.  
 CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 CC Multigene family; Microsome; Alternative splicing.  
 CC SIGNAL  
 CC CHAIN 1 26  
 CC FT TRANSMEM 27 531 UDP-GLUCURONOSYLTRANSFERASE 1-6.  
 CC FT CARBOHYD 293 293 POTENTIAL.  
 CC FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CONFLICT 69 69 K -> G (IN REF. 3).  
 CC FT CONFLICT 104 104 E -> R (IN REF. 3).  
 CC FT CONFLICT 104 104 S -> L (IN REF. 3).

FT CONFLICT 225 225 L -> P (IN REF. 3).  
 FT CONFLICT 466 466 H -> K (IN REF. 2).  
 SQ SEQUENCE 531 AA; 60438 MW; AE7CASF5818DC12 CRC64;

Query Match 2.1%; Score 11; DB 1; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 0.0035;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLDGPKT 366  
 Db 354 PONDLDGPKT 364

RESULT 23  
 ID12\_MOUSE STANDARD; PRT; 533 AA.  
 AC P70691;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 DE (UDPCT) (UGT1\*0) (UGT1-02) (UGT1.2) (UGT1A2) (BILIRUBIN SPECIFIC).  
 GN UGT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=95408245; PubMed=7677729;  
 RA Koike O., Hasada K., Yasui Y., Sakai Y., Sato H., Watanabe T.;  
 RT "Isolation of cDNAs for mouse phenol and bilirubin UDP-  
 RT glucuronosyltransferase and mapping of the mouse gene for phenol  
 RT UDP-glucuronosyltransferase (Ugt1a) to chromosome 1 by restriction  
 RT fragment length variations";  
 RL Biochem. Genet. 33:111-122(1995).  
 CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR =  
 CC UDP + ACCEPTOR BETA-D-GLUCURONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: D87866; BAA13482.1; -  
 CC MGD: MGI:98898; Ugt1a1.  
 CC InterPro: IPR002213; -  
 CC Pfam: PF00201; UDPCT; 1.  
 CC PROSITE: PS00375; UDPCT; 1.  
 CC Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 CC Multigene family; Microsome; Alternative splicing.  
 CC SIGNAL  
 CC CHAIN 1 27  
 CC FT TRANSMEM 28 533 UDP-GLUCURONOSYLTRANSFERASE 1-2.  
 CC FT CARBOHYD 491 511 POTENTIAL.  
 CC FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 533 AA; 60285 MW; FB45843952550FA CRC64;

Query Match 2.1%; Score 11; DB 1; Length 533;  
 Best Local Similarity 100.0%; Pred. No. 0.0035;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 366  
 |||||||||  
 Db 356 PONDGLGHPK 366

## RESULT 24

ID UD16\_RAT STANDARD; PRT: 529 AA.

AC P08430;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)

DE (UDPGT) (UGT1\*6) (UGT1-06) (UGT1A6) (A1) (P-NITROPHENOL SPECIFIC).

GN UGT1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RP STRAIN-WISTAR;

RX MEDLINE=87057193; PubMed=3096993;

RA Iyanagi T., Hanu M., Sogawa K., Fujii-Kuriyama Y., Watanabe S.,

RA Shively J.E., Anan K.F.;

RT "Cloning and characterization of cDNA encoding 3-methylcholanthrene

RT inducible rat mRNA for UDP-glucuronosyltransferase.";

RL J. Biol. Chem. 261:15607-15614(1986)

CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS.

CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR

CC BETA-D-GLUCURONOSIDE.

CC -1- SUBCELLULAR LOCATION: MICROSOMAL.

CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT

CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A

CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.

CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.

CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.

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CC -----

DR EMBL: J02612; AAA42311.1; -

DR PIR: A24600; A24600.

DR InterPro: IPR002213; -

DR Pfam: PF00201; UDPGT: 1.

DR PROSITE: PS00375; UDPGT: 1.

KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;

KW Multigene family; Microsome; Alternative splicing.

KW SIGNAL

FT CHAIN 1 25 UDP-GLUCURONOSYLTRANSFERASE 1-6.

FT TRANSMEM 26 529 POTENTIAL.

FT CARBOHYD 281 281 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT CARBOHYD 291 291 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT CARBOHYD 429 429 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT SEQUENCE 529 AA; 60132 MW; 14AACDA7EDDE04B CRC64;

QY 356 PONDGLGHPK 365

Query Match 1.9%; Score 10; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 352 PONDGLGHPK 361  
 |||||||||

## RESULT 25

ID UD18\_RAT STANDARD; PRT: 530 AA.

AC Q64634;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE UDP-GLUCURONOSYLTRANSFERASE 1-8 PRECURSOR, MICROSOMAL (EC 2.4.1.17)

DE (UDPGT) (UGT1\*8) (UGT1-08) (UGT1A8) (A3).

GN UGT1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RP STRAIN-WISTAR;

RX MEDLINE=95332265; PubMed=7608130;

RA Eml Y., Ikushiro S.I., Iyanagi T.;

RT "Drug-responsive and tissue-specific alternative expression of 1

RT multiple first exons in rat UDP-glucuronosyltransferase family 1

RT (UGT1) gene complex.";

RL J. Biochem. 117:392-399(1995).

CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS.

CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR

CC BETA-D-GLUCURONOSIDE.

CC -1- SUBCELLULAR LOCATION: MICROSOMAL.

CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT

CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A

CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.

CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.

CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.

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CC -----

DR EMBL: D38063; BA07259.1; -

DR PIR: M34007; AAA42312.1; ALT-TERM.

DR InterPro: IPR002213; -

DR Pfam: PF00201; UDPGT: 1.

DR PROSITE: PS00375; UDPGT: 1.

KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;

KW Multigene family; Microsome; Alternative splicing.

KW SIGNAL

FT CHAIN 1 25 UDP-GLUCURONOSYLTRANSFERASE 1-8.

FT TRANSMEM 26 530 POTENTIAL.

FT CARBOHYD 488 504 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT CARBOHYD 71 71 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT CARBOHYD 292 292 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT CARBOHYD 430 430 N-LINKED (GLCNAAC... ) (POTENTIAL).

FT SEQUENCE 530 AA; 60060 MW; 507098A8E81D4AC5C CRC64;

QY 356 PONDGLGHPK 365

Query Match 1.9%; Score 10; DB 1; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 356 PQNDLGHPR 365  
 |||||  
 Db 353 PQNDLGHPR 362

RESULT 26  
 ID U013\_RAT STANDARD: PRT: 531 AA.  
 AC 064637;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 GN (UDPCT) (UGT1\*3) (UGT1-03) (UGT1A3) (B5).  
 GN UGT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-286 FROM N.A.  
 RC STRAIN-WISTAR;  
 RX MEDLINE=95332265; PubMed=7608130;  
 RA Emi Y., Ikushiro S.I., Iyanagi T.;  
 RT "Drug-responsive and tissue-specific alternative expression of  
 multiple first exons in rat UDP-glucuronosyltransferase family 1  
 (UGT1) gene complex.";  
 RL J. Biochem. 117:392-399(1995).  
 RN [2]  
 RP SEQUENCE OF 287-531 FROM N.A.  
 RC TISSUE-Liver;  
 RX MEDLINE=90274676; PubMed=2112380;  
 RA Sato H., Koike O., Tanabe K., Kashiwamata S.;  
 RT "Isolation and sequencing of rat liver bilirubin UDP-  
 glucuronosyltransferase cDNA: possible alternate splicing of a common  
 primary transcript.";  
 RL Biochem. Biophys. Res. Commun. 169:260-264(1990).  
 RN [1]  
 RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCORONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: D38067; BAA07262.1; -  
 CC EMBL: M34007; AAA42312.1; ALT\_TERM.  
 CC InterPro: IPR002213; -  
 CC Pfam: PF00201; UDPGT; 1.  
 CC PROSITE: PS00375; UDPGT; 1.  
 CC Transfaser: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 CC Multigene family; Microsome; Alternative splicing.  
 CC SIGNAL 1 25  
 CC UDP-GLUCURONOSYLTRANSFERASE 1-3.  
 CC POTENTIAL.  
 CC CHAIN 26 531  
 CC TRANSFERASE 489 505  
 CC CARBOHYD 116 139  
 CC FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 531 AA: 60140 MW; ECB0994CA62AC7CEFCRC64;

Query Match 1.9%; Score 10; DB 1; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PQNDLGHPR 365  
 |||||  
 Db 354 PQNDLGHPR 363

RESULT 27  
 ID U015\_RAT STANDARD: PRT: 531 AA.  
 AC 064638;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE UDP-GLUCURONOSYLTRANSFERASE 1-5 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
 GN (UDPCT) (UGT1\*5) (UGT1-05) (UGT1A5) (B5).  
 GN UGT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-286 FROM N.A.  
 RC STRAIN-WISTAR;  
 RX MEDLINE=95332265; PubMed=7608130;  
 RA Emi Y., Ikushiro S.I., Iyanagi T.;  
 RT "Drug-responsive and tissue-specific alternative expression of  
 multiple first exons in rat UDP-glucuronosyltransferase family 1  
 (UGT1) gene complex.";  
 RL J. Biochem. 117:392-399(1995).  
 RN [2]  
 RP SEQUENCE OF 287-531 FROM N.A.  
 RC TISSUE-Liver;  
 RX MEDLINE=90274676; PubMed=2112380;  
 RA Sato H., Koike O., Tanabe K., Kashiwamata S.;  
 RT "Isolation and sequencing of rat liver bilirubin UDP-  
 glucuronosyltransferase cDNA: possible alternate splicing of a common  
 primary transcript.";  
 RL Biochem. Biophys. Res. Commun. 169:260-264(1990).  
 RN [1]  
 RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 ENDGENOUS COMPOUNDS.  
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
 CC BETA-D-GLUCORONOSIDE.  
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
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 CC -----  
 CC EMBL: D38069; BAA07263.1; -  
 CC EMBL: M34007; AAA42312.1; ALT\_TERM.  
 CC InterPro: IPR002213; -  
 CC Pfam: PF00201; UDPGT; 1.  
 CC PROSITE: PS00375; UDPGT; 1.  
 CC Transfaser: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
 CC Multigene family; Microsome; Alternative splicing.  
 CC SIGNAL 1 25  
 CC UDP-GLUCURONOSYLTRANSFERASE 1-5.  
 CC CHAIN 26 531  
 CC TRANSFERASE 489 505  
 CC CARBOHYD 116 116  
 CC FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 531 AA; 59993 MW; 04148C1BACAC80 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365
DB 354 PONDLLGHPK 363
```

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RESULT 28
UD12_RAT
ID UD12_RAT STANDARD; PRT; 531 AA.
AC 064633;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPCT) (UGT1*7) (UGT1-07) (UGT1A7) (A2).
GN UGT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-286 FROM N.A.
RC STRAIN=Wistar;
RC MEDLINE=95332265; PubMed=7608130;
RA Emi Y., Ikushiro S.I., Iyanagi T.;
RT "Drug-responsive and tissue-specific alternative expression of
RT multiple first exons in rat UDP-glucuronosyltransferase family 1
RT (UGT1) gene complex.";
RT J. Biochem. 117:392-399(1995).
RN [2]
RP SEQUENCE OF 287-531 FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=90274676; PubMed=2112380;
RA Sato H., Koizumi O., Tanabe K., Kashimawata S.;
RT "Isolation and sequencing of rat liver bilirubin UDP-
RT glucuronosyltransferase cDNA: possible alternate splicing of a common
RT primary transcript.";
RL Biochem. Biophys. Res. Commun. 169:260-264(1990).
RL - FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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CC -----
CC EMBL: D38062; BAA07258.1; -
CC EMBL: M34007; AAA42312.1; ALT_TERM.
CC InterPro: IPR002213; -
CC Pfam: PF00201; UDPGT; 1.
CC PROSITE: PS00375; UDPGT; 1.
CC Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
```

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KW Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 531 UDP-GLUCURONOSYLTRANSFERASE 1-7.
FT TRANSMEM 487 503 POTENTIAL.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 531 AA; 59627 MW; BC791DEC724CA621 CRC64;
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Query Match 1.9%; Score 10; DB 1; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365
DB 354 PONDLLGHPK 363
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```
RESULT 29
UD12_RAT
ID UD12_RAT STANDARD; PRT; 533 AA.
AC P20720; 064636;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPCT) (UGT1*0) (UGT1-02) (UGT1A2) (BILIRUBIN SPECIFIC)
DE (B2).
GN UGT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=90274676; PubMed=2112380;
RA Sato H., Koizumi O., Tanabe K., Kashimawata S.;
RT "Isolation and sequencing of rat liver bilirubin UDP-
RT glucuronosyltransferase cDNA: possible alternate splicing of a common
RT primary transcript.";
RL Biochem. Biophys. Res. Commun. 169:260-264(1990).
RN [2]
RP SEQUENCE OF 1-288 FROM N.A.
RC STRAIN=Wistar;
RC MEDLINE=95332265; PubMed=7608130;
RA Emi Y., Ikushiro S.I., Iyanagi T.;
RT "Drug-responsive and tissue-specific alternative expression of
RT multiple first exons in rat UDP-glucuronosyltransferase family 1
RT (UGT1) gene complex.";
RT J. Biochem. 117:392-399(1995).
RL - FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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CC -----
CC EMBL: M34007; AAA42312.1; -
CC EMBL: D38066; BAA07261.1; -
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DR PIR: A35343; A35343.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1 27
FT CHAIN 28 533
FT TRANSFER 491 507
FT CARBOHYD 133 133
FT CARBOHYD 141 141
FT CARBOHYD 295 295
FT CARBOHYD 433 433
FT CONFLICT 2 3
FT CONFLICT 177 178
SQ SEQUENCE 533 AA; 60045 MW; 5A9E974EF7EBAF5B CRC64;

Query Match
Best Local Similarity 1.9%; Score 10; DB 1; Length 533;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 365
DB 356 PONDGLGHPK 365

RESULT 30
UD11_RAT
ID UD11_RAT STANDARD; PRT; 535 AA.
AC 064550; 064635;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1*1) (UGT1-01) (UGT1A1) (BL).
GN UGT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95327065; PubMed=7603447;
RA Coffman B.L., Green M.D., King C.O., Tephly T.R.;
RT "Cloning and stable expression of a cDNA encoding a rat liver UDP-
RT glucuronosyltransferase (UDP-glucuronosyltransferase 1.1) that
RT catalyzes the glucuronidation of opioids and bilirubin."
RL Mol. Pharmacol. 47:1101-1105(1995).
RN [2]
RP SEQUENCE OF 1-290 FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95332265; PubMed=7608130;
RA Eml Y., Iwashiro S.I., Iyanagi T.;
RT "Drug-responsive and tissue-specific alternative expression of
RT multiple first exons in rat UDP-glucuronosyltransferase family 1
RT (UGT1) gene complex."
RL J. Biochem. 117:392-399(1995).
RN [3]
RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
RN SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
RN ENDOGENOUS COMPOUNDS. GLUCURONATES OPIOIDS AND BILIRUBIN.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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CC -----
DR EMBL: U20551; AAC52219.1; -.
DR EMBL: D38065; BAA07260.1; -.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR Transferrase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 535
FT TRANSFER 493 509
FT CARBOHYD 89 89
FT CARBOHYD 297 297
FT CARBOHYD 435 435
FT CONFLICT 253 253
SQ SEQUENCE 535 AA; 59662 MW; 26B642FCA7DD4082 CRC64;

Query Match
Best Local Similarity 1.9%; Score 10; DB 1; Length 535;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDGLGHPK 365
DB 358 PONDGLGHPK 367

RESULT 31
UD17_MOUSE
ID UD17_MOUSE STANDARD; PRT; 520 AA.
AC 062452;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1*7) (UGT1-07) (UGT1A7) (UGT1A4) (FRAGMENT).
GN UGT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=93219265; PubMed=8464825;
RA Kong A.N., Ma M., Tao D., Yang L.;
RT "Molecular cloning of two cDNAs encoding the mouse bilirubin/phenol
RT family of UDP-glucuronosyltransferases (mUGTbr/P).";
RL Pharm. Res. 10:461-465(1993).
RN [2]
RP FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
RN SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
RN ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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CC -----
DR EMBL: L27122; AAA40524.1; ALT_INT.

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DR MGD: MGI:98898; Ugt1a1.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KM Multigene family; Microsome; Alternative splicing.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 1
FT TRANSMEM 16 520 UDP-GLUCURONOSYLTRANSFERASE 1-7.
FT CARBOHYD 61 494 POTENTIAL.
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 520 AA; 59193 MW; 2048D5C5CDAC895 CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 1; Length 520;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 301 GIVFSLGS 309
|||||
Db 288 GIVFSLGS 296

RESULT 32
ID ID12_HUMAN STANDARD; PRT; 530 AA.
AC P36509;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-2 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1-1B) (UGT1-02) (UGT1A2) (UGT1B)
DE (HLUGP4).
GN UGT1 OR GNT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91378895; PubMed=1910331;
RA Wooster R., Sutherland L., Ebner T., Clarke D., E Silva O.,
RA Burchell B.;
RT "Cloning and stable expression of a new member of the human liver
RT phenol/bilirubin: UDP-glucuronosyltransferase cDNA family.";
RT Biochem. J. 278:465-469(1991).
RN [2]
RP SEQUENCE OF 286-530 FROM N.A.
RX MEDLINE=92147680; PubMed=1339448;
RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,
RA Owens I.S.;
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and
RT other UDP-glucuronosyltransferase isozymes with identical carboxyl
RT terminl.";
RL J. Biol. Chem. 267:3257-3261(1992).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S55985; AAB19791.2; -.
DR PIR: S17512; S17512.
DR MIM: 191740; -.
DR InterPro: IPR002213; -.
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KM Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1
FT CHAIN 1
FT TRANSMEM 26 530 UDP-GLUCURONOSYLTRANSFERASE 1-2.
FT CARBOHYD 292 504 POTENTIAL.
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 301 301 V -> G (IN REF. 1).
FT CONFLICT 340 340 S -> C (IN REF. 1).
FT CONFLICT 364 364 R -> S (IN REF. 1).
FT CONFLICT 410 410 L -> M (IN REF. 1).
FT CONFLICT 419 419 D -> E (IN REF. 1).
FT CONFLICT 469 469 P -> T (IN REF. 1).
FT CONFLICT 495 495 V -> A (IN REF. 1).
FT CONFLICT 504 504 F -> C (IN REF. 1).
FT SEQUENCE 530 AA; 60018 MW; 9075B002010B67CE CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 1; Length 530;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 301 GIVFSLGS 309
|||||
Db 298 GIVFSLGS 306

RESULT 33
ID ID16_HUMAN STANDARD; PRT; 531 AA.
AC P19224;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1-1F) (UGT1-06) (UGT1A6) (UGT1F) (PHENOL
DE SPECIFIC).
GN UGT1 OR GNT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92147680; PubMed=1339448;
RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,
RA Owens I.S.;
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and
RT other UDP-glucuronosyltransferase isozymes with identical carboxyl
RT terminl.";
RL J. Biol. Chem. 267:3257-3261(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89042187; PubMed=3141926;
RA Harding D., Fournel-gigleux S., Jackson M.R., Burchell B.;
RT "Cloning and substrate specificity of a human phenol UDP-
RT glucuronosyltransferase expressed in COS-7 cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:8381-8385(1988).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
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CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M84130; AAC41717.1; -
DR EMBL: M84124; AAA61247.1; ALT SEQ.
DR EMBL: M84122; AAA61247.1; JOINED.
DR EMBL: M84123; AAA61247.1; JOINED.
DR EMBL: J04093; AAA61251.1; -
DR PIR: A31340; AAA61251.1; -
DR MIM: A31340; A31340.
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR TRANSFERASE: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
DR Multigene family: Microsome; Alternative splicing.
DR SIGNAL: 1
DR CHAIN: 1
DR TRANSMEM: 531
DR CARBOHYD: 489 505
DR FT CARBOHYD 293 293 N-LINKED (GLCNC. . .) (POTENTIAL).
DR FT CARBOHYD 345 345 N-LINKED (GLCNC. . .) (POTENTIAL).
DR FT CONFLICT 70 70 Y -> S (IN REF. 2).
DR FT CONFLICT 231 231 K -> E (IN REF. 2).
DR FT CONFLICT 247 248 SE -> YOK (IN REF. 2).
DR FT CONFLICT 327 327 N -> I (IN REF. 2).
DR FT CONFLICT 509 509 P -> A (IN REF. 2).
DR FT CONFLICT 513 513 P -> R (IN REF. 2).
DR SEQUENCE 531 AA: 60590 MW: AA62AD6DFPAC823C CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 1; Length 531;
Matches 9; Conservative 0; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
DB 299 GIVFSLGS 307

RESULT 34
UD16_RABIT STANDARD: PRT: 531 AA.
AC 028611:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-6 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1*6) (UGT1-06) (UGT1A6).
DE UGT1.
GN Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
OX [1]
RN SEQUENCE FROM N.A. AND CHARACTERIZATION.
RP STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
RX MEDLINE=84347791; PubMed=808691;
RA Lamb J.G., Straub P., Tukey R.H.;
RT Cloning and characterization of cDNAs encoding mouse Ugt1.6 and
RT rabbit Ugt1.6: differential induction by
RT 2,3,7,8-tetrachlorodibenzo-p-dioxin.
RL Biochemistry 33:10513-10520(1994).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

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CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS. CONJUGATES SMALL PLANAR PHENOLIC MOLECULES
CC SUCH AS 4-NITROPHENOL, 1-NAPHTHOL, AND 4-METHYLBELLIFERONE. THE
CC BULKY PHENOL 4-HYDROXYBIPHENYL, ANDROGENS AND ESTROGENS ARE NOT
CC SUBSTRATES. 2-HYDROXYBIPHENYL IS AN EXCELLENT SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES (BY SIMILARITY).
CC -1- INDUCTION: BY DIOXIN.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSYLTRANSFERASE FAMILY.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U09030; AAA51867.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR TRANSFERASE: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
DR Multigene family: Microsome; Alternative splicing.
DR SIGNAL: 1
DR CHAIN: 26
DR TRANSMEM: 27 531
DR CARBOHYD: 489 505 N-LINKED (GLCNC. . .) (POTENTIAL).
DR FT CARBOHYD 294 294
DR SEQUENCE 531 AA: 60098 MW: 872D317852F0928F CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 1; Length 531;
Matches 9; Conservative 0; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
DB 300 GIVFSLGS 308

RESULT 35
UD14_RABIT STANDARD: PRT: 532 AA.
AC 028612:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE UDP-GLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
DE (UDPGT) (UGT1*4) (UGT1-04) (UGT1A4).
DE UGT1.
GN Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
RA Philipp T., Durazzo M., Trautwein C., Alex B., Johnson E.F.,
RA Straub J.G., Straub P., Tukey R.H., Manns M.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES (BY SIMILARITY).
CC

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RT syndrome, type I." ;  
 RL FASEB J. 6:2859-2863(1992).  
 RN [4]  
 RP VARIANTS CN-II ARG-71 AND ASP-486.  
 RX MEDLINE=941073323; PubMed=8280139;  
 RA Aono S., Yamada Y., Keino H., Hanada N., Nakagawa T., Sasaoka Y.,  
 RT Yawara I., Sato H., Koikei O.;  
 RL "Identification of defect in the genes for bilirubin UDP-glucuronosyl  
 RT transferase in a patient with Crigler-Najjar syndrome type II." ;  
 RL Biochem. Biophys. Res. Commun. 197:1239-1244(1993).  
 RN [5]  
 RP VARIANT CN-II ARG-331.  
 RX MEDLINE=94102756; PubMed=8276413;  
 RA Moghrabi N., Clarke D.J., Boxer M., Burchell B.;  
 RL "Identification of an A-to-G missense mutation in exon 2 of the UGT1  
 RT gene complex that causes Crigler-Najjar syndrome type 2." ;  
 RL Genomics. 18:171-173(1993).  
 RN [6]  
 RP VARIANT CN-I PHE-170 DEL.  
 RX MEDLINE=94043159; PubMed=8226884;  
 RA Ralzer J.K., Yeaman M.T., Kaiser C., Gridelli B., Owens I.S.;  
 RL "A phenylalanine codon deletion at the UGT1 gene complex locus of a  
 RT Crigler-Najjar type I patient generates a pH-sensitive bilirubin UDP-  
 RL glucuronosyltransferase." ;  
 RL J. Biol. Chem. 268:23573-23579(1993).  
 RN [7]  
 RP VARIANTS CN-I V-292; E-308; R-357; T-368; R-381; P-401 AND E-428.  
 RX MEDLINE=95080780; PubMed=7989045;  
 RA Labrune P., Myara A., Hadchouel M., Ronchi F., Bernard O., Trivin F.,  
 RL Roy Chowdhury N., Roy Chowdhury J., Munnich A., Odievle M.;  
 RT "Genetic heterogeneity of Crigler-Najjar syndrome type I: a study of  
 RT 14 cases." ;  
 RL Hum. Genet. 94:693-697(1994).  
 RN [8]  
 RP VARIANTS CN G1U-175; ARG-177; TRP-209; ARG-276 AND PHE-375.  
 RX MEDLINE=95081424; PubMed=7969595;  
 RA Seppen J., Bosma P.J., Goldhoorn B.G., Bakker C.T.M.,  
 RL Roy Chowdhury J., Roy Chowdhury N., Jansen P.L.M.,  
 RT Oude Elferink R.P.J.;  
 RT "Discrimination between Crigler-Najjar type I and II by expression of  
 RT mutant bilirubin uridine diphosphate glucuronosyltransferase." ;  
 RL J. Clin. Invest. 94:2385-2391(1994).  
 RN [9]  
 RP VARIANTS CN II ARG-71; TRP-209; G1U-229 AND ASP-486.  
 RX MEDLINE=98284535; PubMed=9621515;  
 RA Yamamoto K., Soeda Y., Kamisako T., Hosaka H., Fukano M., Sato H.,  
 RL Fujiyama Y., Dachi Y., Satoh N., Bamba T.;  
 RT "Analysis of bilirubin uridine 5'-diphosphate (UDP)-  
 RT glucuronosyltransferase gene mutations in seven patients with Crigler  
 RT Najjar syndrome type II." ;  
 RL J. Hum. Genet. 43:111-114(1998).  
 RN [10]  
 RP VARIANT GILBERT SYNDROME ASP-486.  
 RX MEDLINE=98291073; PubMed=9627603;  
 RA Maruo Y., Sato H., Yamano T., Doiwa Y., Shimada M.;  
 RL "Gilbert syndrome caused by a homozygous missense mutation (Tyr486Asp)  
 RT of bilirubin UDP-glucuronosyltransferase gene." ;  
 RL J. Pediatr. 132:1045-1047(1998).  
 CC -I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
 CC ENDOGENOUS COMPOUNDS. GLUCURONIDATES BILIRUBIN IX-ALPHA TO FORM  
 CC BOTH THE IX-ALPHA-C8 AND IX-ALPHA-C12 MONOCONJUGATES AND  
 CC DICONGUGATE.  
 CC -I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR - UDP + ACCEPTOR  
 CC BETA-D-GLUCORONOSIDE.  
 CC -I- SUBCELLULAR LOCATION: MICROSOMAL.  
 CC -I- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
 CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
 CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
 CC -I- DISEASE: THE GILBERT'S SYNDROME IS SHOWN TO OCCUR AS A CONSEQUENCE  
 CC OF REDUCED BILIRUBIN TRANSFERASE ACTIVITY. THE DISORDER, IS MOST  
 CC OFTEN DETECTED IN YOUNG ADULTS WITH VAGUE NONSPECIFIC COMPLAINTS.  
 CC A MORE SEVERE INHERITABLE DEFICIENCY IN BILIRUBIN ACTIVITY EXIST

FT	VARIANT	486	486	/FTID=VAR_007708; Y->D (IN CRIGLER-NAIJAR TYPE II AND GILBERT SYNDROME). /FTID=VAR_007709.
FT	PT			
SQ	SEQUENCE	533 AA;	59591 MW;	19C90231AD0EB547 CRC64;
Qy	Query Match	301 GIYVFSLGS 309	1.7%;	Score 9; DB 1; Length 533;
	Best Local Similarity	100.0%;	Pred No. 0.41;	
Matches	9; Conservative	0; Mismatches	0; Indels	0; Gaps
Db	301 GIYVFSLGS 309			0
RESULT 37				
UD13 HUMAN				
ID UD13_HUMAN	STANDARD;	PRT;	534 AA.	
AC P35503;				
DT 01-JUN-1994 (Rel. 29, Created)				
DT 01-JUN-1994 (Rel. 29, Last sequence update)				
DT 01-NOV-1997 (Rel. 35, Last annotation update)				
DE UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICROSOAL (EC 2.4.1.17)				
DE (UDPCT) (UGT1-1C) (UGT1*3) (UGT1-03) (UGT1A3) (UGT1C).				
GN UGT1 OR GMT1				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
NCHI_TaxID=9606;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=92147680; PubMed=1339448;				
RA Ritter J.K., Chen F., Sheen Y.X., Tran H.M., Kimura S., Yeatman M.T.,				
Owens I.S.;				
* A novel complex locus UGT1 encodes human bilirubin, phenol, and				
other UDP-glucuronosyltransferase isozymes with identical carboxyl				
termini.";				
RL J. Biol. Chem. 267:3257-3261(1992).				
-I FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND				
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND				
ENOGENOUS COMPOUNDS.				
-I CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR				
BETA-D-GLUCONOSIDE.				
-I SUBCELLULAR LOCATION: MICROSOAL.				
-I ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT				
UDPCT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A				
COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.				
-I SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.				
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-----				
CC EMBL; M84127; AAA92020.1; -				
DR EMBL; M84124; AAA61247.1; ALT_SEQ.				
DR EMBL; M84123; AAA61247.1; JOINED.				
DR EMBL; M84123; AAA61247.1; JOINED.				
MIM; 191740; -				
DR InterPro; IPRO02213; -				
DR Pfam; PF00201; UDPGT; 1.				
DR PROSITE; PS00375; UDPGT; 1.				
KW Transferase; Glycosyltransferase; glycoprotein; Transmembrane; Signal;				
Multiene family; Microsome; Alternative splicing.				
FT SIGNAL	1	28	POTENTIAL.	
FT CHAIN	492	534	POTENTIAL.	
FT TRANSMEM	292	508	POTENTIAL.	
FT CARBOHYD	119	119	N-LINKED (GLCNAC. . . ) (POTENTIAL).	
FT CARBOHYD	142	142	POTENTIAL.	
FT				

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 534 AA: 60338 MW: 9C5833652A4D9B3D CRC64;  
  
Query Match 1.7%; Score 9; DB 1; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 301 GIVFSLGS 309  
Db 302 GIVFSLGS 310  
  
RESULT 38  
UD14\_HUMAN  
ID UD14\_HUMAN STANDARD: PRT: 534 AA.  
AC P22310;  
DT 01-AUG-1991 (Rel. 19, created)  
DT 01-AUG-1991 (Rel. 19, last sequence update)  
DT 01-OCT-2000 (Rel. 40, last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-4 PRECURSOR, MICROSOFT (EC 2.4.1.17)  
DE (UDPGLT) (UGT-1D) (UGT1-4) (UGT1A4) (UGT1D)  
DE (BILIRUBIN SPECIFIC ISOZYME 2) (HUG-BR2).  
GN UGT1 OR GNT1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=91093210; PubMed=1898728;  
RT Rittner J.K., Crawford J.M., Owens I.S.;  
RT "Cloning of two human liver bilirubin UDP-glucuronosyltransferase  
RL CDNA with expression in COS-1 cells.";  
RL J. Biol. Chem. 266:1043-1047(1991).  
RN [2]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RX MEDLINE=92147680; PubMed=1339448;  
RT Rittner J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,  
RA Owens I.S.;  
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and  
RL other UDP-glucuronosyltransferase isozymes with identical carboxyl  
termini.";  
RL J. Biol. Chem. 267:3257-3261(1992).  
RN [3]  
RP VARIANT CN-I PHE-376.  
RX MEDLINE=92339803; PubMed=1634050;  
RA Bosma P.J., Chowdhury J.R., Huang T.-J., Lahiri P., Elfeink R.P.J.O.,  
RA van Es H.H.G., Lederstein M., Whittington P.F., Jansen P.L.,  
RA Chowdhury N.R.;  
RT "Mechanisms of inherited deficiencies of multiple UDP-  
RT glucuronosyltransferase isoforms in two patients with Crigler-Najjar  
RL syndrome, type I.";  
RL PASEB J. 6:2859-2863(1992).  
RN [4]  
RP VARIANTS CN-II PRO-132 AND ASP-487.  
RX MEDLINE=94107323; PubMed=8280139;  
RA Aono S., Yamada Y., Kellno H., Hanada N., Nakagawa T., Sasaoka Y.,  
RA Yawata T., Sato H., Koiwai O.;  
RT "Identification of defect in the genes for bilirubin UDP-glucuronosyl-  
RT transferase in a patient with Crigler-Najjar syndrome type II.";  
RL Biochem. Biophys. Res. Commun. 197:1239-1244(1993).  
RN [5]  
RP VARIANT CN-II ARG-332.  
RX MEDLINE=94102756; PubMed=8276413;  
RA Moghribi N., Clarke D.J., Boxer M., Burchell B.;  
RT "Identification of an A-to-G missense mutation in exon 2 of the UGT1  
RL gene complex that causes Crigler-Najjar syndrome type 2.";  
CC -1- FUNCTION: UDPGLT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS, GLUCURONIDATES BILIRUBIN IX-ALPHA TO FORM  
CC BOTH THE IX-ALPHA-C8 AND IX-ALPHA-C12 MONOCONJUGATES AND  
CC DISCONJUGATE.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOFT.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER. NOT EXPRESSED IN SKIN OR  
CC KIDNEY.  
CC -1- INDUCTION: BY PHENOBARBITAL.  
CC -1- DISEASE: THE GILBERT'S SYNDROME IS SHOWN TO OCCUR AS A CONSEQUENCE  
CC OF REDUCED BILIRUBIN TRANSFERASE ACTIVITY. THE DISORDER, IS MOST  
CC OFTEN DETECTED IN YOUNG ADULTS WITH VAGUE NONSPECIFIC COMPLAINTS.  
CC A MORE SEVERE INHERITABLE DEFICIENCY IN BILIRUBIN ACTIVITY EXIST  
CC IN CRIGLER-NAJJAR (CN): PATIENTS WITH TYPE I (RECESSIVE TRAIT)  
CC HAVE SEVERE HYPERBILIRUBINEMIA AND USUALLY DIE OF KERNICTERUS  
CC (BILIRUBIN ACCUMULATION IN THE BASAL GANGLIA AND BRAINSTEM NUCLEI)  
CC WITHIN THE FIRST YEAR OF LIFE. PATIENTS WITH TYPE II (DOMINANT  
CC TRAIT) HAVE LESS SEVERE HYPERBILIRUBINEMIA AND USUALLY SURVIVE  
CC INTO ADULTHOOD WITHOUT NEUROLOGIC DAMAGE. PHENOBARBITAL, WHICH  
CC INDUCES THE PARTIALLY DEFICIENT GLUCURONYL TRANSFERASE, CAN  
CC DIMINISH THE JAUNDICE.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC  
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CC  
CC EMBL: M84128; AAA61249.1; -  
CC EMBL: M84124; AAA61247.1; ALT SEQ.  
CC EMBL: M84123; AAA61247.1; JOINED.  
CC EMBL: M57951; AAA63196.1; -  
CC PIR: B39092; B39092.  
CC MIM: 191740; -  
CC MIM: 143500; -  
CC MIM: 218800; -  
CC InterPro: IPR002213; -  
CC Pfam: PF00201; UDPGT; 1.  
CC PROSITE: PS00375; UDPGT; 1.  
CC DR Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
CC KW Multigene family; Microsome; Alternative splicing; Disease mutation.  
CC FT SIGNAL 1 28  
FT CHAIN 29 534  
FT TRANSMEM 492 508  
FT CARBOHYD 119 119  
FT CARBOHYD 142 142  
FT CARBOHYD 296 296  
FT CARBOHYD 348 348  
FT VARIANT 132 132  
FT VARIANT 332 332  
FT VARIANT 376 376  
FT VARIANT 487 487  
FT SEQUENCE 534 AA: 60025 MW: AB745D46F538BE CRC64;  
  
Query Match 1.7%; Score 9; DB 1; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 301 GIVFSLGS 309  
Db 302 GIVFSLGS 310

RESULT 39  
ID15\_HUMAN STANDARD; PRT; 534 AA.  
AC P35504;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-5 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (UGT1-1E) (UGT1-5) (UGT1A5) (UGT1E).  
GN UGT1 OR GNT1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92147680; PubMed=1339448;  
RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,  
OWENS I.S.;  
RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and  
RT other UDP-glucuronosyltransferase isozymes with identical catalytic  
RT termini.";  
RL J. Biol. Chem. 267:3257-3261(1992).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
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CC  
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DR EMBL: M84129; AAA61250.1; -  
DR EMBL: M84124; AAA61247.1; ALT\_SEQ.  
DR EMBL: M84122; AAA61247.1; JOINED.  
DR EMBL: M84123; AAA61247.1; JOINED.  
DR MIM: 191740;  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Alternative splicing.  
FT SIGNAL 1  
FT CHAIN 29 534 UDP-GLUCURONOSYLTRANSFERASE 1-5.  
FT TRANSMEM 492 508 POTENTIAL.  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 534 AA; 60071 MW; 05989F2A18EFAA4 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309  
|1111111111|  
Db 302 GIVFSLGS 310

RESULT 40

UDP1\_MOUSE  
ID UDP1\_MOUSE STANDARD; PRT; 535 AA.  
AC O63886;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE UDP-GLUCURONOSYLTRANSFERASE 1-1 PRECURSOR, MICROSOMAL (EC 2.4.1.17)  
DE (UDPCT) (UGT1\*1) (UGT1-01) (UGT1A1) (UGTBR1).  
GN UGT1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93219265; PubMed=8464825;  
RA Kong A.N., Ma M., Tao D., Yang L.;  
RT "Molecular cloning of two cDNAs encoding the mouse bilirubin/phenol  
RT family of UDP-glucuronosyltransferases (mUGTBR/p.)."  
RL Pharm. Res. 10:461-465(1993).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROSOMAL.  
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT  
CC UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A  
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.  
CC -1- INDUCTION: BY DIOXIN.  
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC  
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CC  
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DR EMBL: S64760; AA26033.2; -  
DR MGD: MGI:98896; Ugt1a1.  
DR InterPro: IPR002213; -  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;  
KW Multigene family; Microsome; Alternative splicing.  
FT SIGNAL 1  
FT CHAIN 29 535 UDP-GLUCURONOSYLTRANSFERASE 1-1.  
FT TRANSMEM 493 509 POTENTIAL.  
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 535 AA; 60123 MW; B5AE3C209979BBB8 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 535;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309  
|1111111111|  
Db 303 GIVFSLGS 311

RESULT 41  
FER\_BUMFT STANDARD; PRT; 98 AA.  
ID FER\_BUMFT  
AC P13106;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE FERREDOXIN.

```
OS Bumilleropsis filiformis.
OC Eukaryota; Stramenopiles; Xanthophyceae; Bumilleropsis.
OX NCBI_TaxID=2835;
RN [1]
RP SEQUENCE.
RX MEDLINE=84087800; PubMed=6418731;
RA Inoue K., Hase T., Boeger P., Matsubara H.;
RT "Amino acid sequence of a ferredoxin from Bumilleropsis filiformis,
RT a yellow-green alga: relationship with red algae,
RT prochloriellophyceae, and filamentous blue-green algae.";
RT J. Biochem. 94:1451-1455(1983).
CC -1- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
CC ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
CC -1- COFACTOR: BINDS A 2FE-2S CLUSTER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC PIR: A28857; FEBF2.
DR HSSP: P00246; 4FXC.
DR InterPro: IPR000564; -.
DR Pfam: PF00111; Fer2; 1.
DR PRINTS: PR00159; 2FE2S_FERREDOXIN.
DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
KW Electron transport; Iron-sulfur; Chloroplast.
FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 46 46 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 49 49 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT VARIANT 1 1 E -> A.
SQ SEQUENCE 98 AA; 10620 MW; E49CCDAC01DD75E CRC64;

Query Match 1.5%; Score 8; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 493 GFLTCVA 500
DB 74 GFLTCVA 81

RESULT 42
HEM1_CLOJO
ID HEM1_CLOJO STANDARD; PRT; 515 AA.
AC 059292;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.1-) (GLUTR).
GN HEMA.
OS Clostridium josui.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1499;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PERM P-9684;
RX MEDLINE=95394829; PubMed=7665501;
RA Fujino E., Fujino T., Karita S., Sakka K., Ohmiya K.;
RT "Cloning and sequencing of some genes responsible for porphyrin
RT biosynthesis from the anaerobic bacterium Clostridium josui.";
RT J. Bacteriol. 177:5169-5175(1995).
CC -1- FUNCTION: IT MAY BE INVOLVED IN THE SYNTHESIS OF 5-AMINOLEVULINIC
CC ACID (ALA) FROM GLUTAMATE AND IN THAT OF SYROHEME FROM PRECORRIN-
CC 2.
CC -1- CATALYTIC ACTIVITY: GLUTAMYL-TRNA(GLU) + NADPH = GLUTAMATE-1-
CC SEMIALDEHYDE + NADP(+); AND TRNA(GLU).
CC -1- PATHWAY: SYROHEME BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMYL-TRNA REDUCTASE FAMILY.
CC -----
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CC -----
DR EMBL: D28503; BAA05860.1; -.
DR InterPro: IPR000343; -.
DR Pfam: PF00745; GlutR; 1.
DR PROSITE: PS00747; GLUTR; 1.
KW Porphyrin biosynthesis; Oxidoreductase; NADP.
SQ SEQUENCE 515 AA; 58368 MW; A9769824AA30DC4C CRC64;

Query Match 1.5%; Score 8; DB 1; Length 515;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 EIFVDLAL 95
DB 285 EIFVDLAL 292

RESULT 43
CGT_HUMAN
ID CGT_HUMAN STANDARD; PRT; 541 AA.
AC Q16880; 000196;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 2-HYDROXYACETYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR
DE (EC 2.4.1.45) (UDP-GALACTOSE-CERAMIDE GALACTOSYLTRANSFERASE) (CERAMIDE
DE UDP-GALACTOSYLTRANSFERASE) (CEREBROSIDE SYNTHASE).
GN UDP8 OR CGT OR UGT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299661; PubMed=8661025;
RA Bosio A., Binczek E., Lebeau M.M., Fernald A.A., Stoffel W.;
RT "The human gene CGT encoding the UDP-galactose ceramide galactosyl
RT transferase (cerebroside synthase): cloning, characterization, and
RT assignment to human chromosome 4, band q26.";
RT Genomics 34:69-75(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97242209; PubMed=9125199;
RA Kapitonov D.E., Yu R.K.;
RT "Cloning, characterization, and expression of human ceramide
RT galactosyltransferase cDNA.";
RL Biochem. Biophys. Res. Commun. 232:449-453(1997).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY
CC ENZYMAIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
CC ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
CC NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: UDP-GALACTOSE + 2-(2-HYDROXYACETYL)SPHINGOSINE
CC = UDP + 1-(BETA-D-GALACTOSYL)-2-(2-HYDROXYACETYL)SPHINGOSINE.
CC -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDE.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL: U30930; AAC50565.1; -.
DR EMBL: U32370; AAC50815.1; -.
DR EMBL: U31353; AAC50815.1; JOINED.
DR EMBL: U31461; AAC50815.1; JOINED.
DR EMBL: U31658; AAC50815.1; JOINED.
```

RA Coe Zeeze T., Li X., Fujita N., Marcus J., Suzuki K., Francke U.,  
RA Popko B.,  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE. A KEY  
CC ENZYMIC STEP IN THE BIOSYNTHESIS OF GALACTOCEEROSIDES, WHICH  
CC ARE ABUNDANT SPINOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL  
CC NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.  
CC -I- CATALYTIC ACTIVITY: UDP-GALACTOSE + 2-(2-HYDROXYACYL)SPHINGOSINE  
CC = UDP + 1-(BETA-D-GALACTOSYL)-2-(2-HYDROXYACYL)SPHINGOSINE.  
CC -I- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF GALACTOCEEROSIDE.  
CC -I- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.  
CC  
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CC -----

ID	CGT_RAT	STANDARD;	PRT;	541 AA.
AC	009426;			
DT	01-NOV-1995 (rel. 32, Created)			
DT	01-NOV-1995 (rel. 32, Last sequence update)			
DT	01-OCT-2000 (rel. 40, Last annotation update)			
DE	2-HYDROXYACETYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR			
DE	(EC 2.4.1.45) (UDP-GALACTOSE-CERAMIDE GALACTOSYLTRANSFERASE) (CERAMIDE			
DE	UDP-GALACTOSYLTRANSFERASE) (CEREBROSIDE SYNTHASE).			
GN	UGT8 OR CGT OR UGT4.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Brain;			
RC	MEDLINE=94052143; PubMed=7694285;			
RT	Schulte S., Stoffel W.;			
RT	"Ceramide UDPgalactosyltransferase from myelinating rat brain:			
RT	purification, cloning, and expression."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:10265-10269(1993).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;			
RC	MEDLINE=94358923; PubMed=7521399;			
RA	Stahl N., Jurevics H., Morell P., Suzuki K., Popko B.;			
RT	"Isolation, characterization, and expression of cDNA clones that			
RT	encode rat UDP-galactose: ceramide galactosyltransferase."			
RL	J. Neurosci. Res. 38:234-242(1994).			
RT	-1- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE. A KEY			



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CC      ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
CC      ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
CC      NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC      -1- CATALYTIC ACTIVITY: UDP-GALACTOSE + 2-(2-HYDROXYACYL)SPHINGOSINE
CC      = UDP + 1-(BETA-D-GALACTOSYL)-2-(2-HYDROXYACYL)SPHINGOSINE.
CC      -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDE.
CC      -1- TISSUE SPECIFICITY: BRAIN, RESTRICTED TO THE OLIGODENDROCYTE-
CC      CONTAINING CELL LAYERS OF CEREBRUM AND CEREBELLUM.
CC      -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC      -----
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CC      -----
DR      EMBL; L21698; AAA16108.1; -.
DR      EMBL; U07683; AAA50212.1; -.
DR      InterPro; IPR002213; -.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW      Microsome.
FT      SIGNAL      1      20      POTENTIAL.
FT      CHAIN      21      541      2-HYDROXYACYLSPHINGOSINE 1-BETA-
FT      TRANSMEM      472      492      GALACTOSYLTRANSFERASE.
FT      CARBOHYD      78      78      POTENTIAL.
FT      CARBOHYD      333      333      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      442      442      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      SEQUENCE      541 AA; 61126 MW; 260D7603170151BB CRC64;
OY      356 PONDILGH 363
DB      342 PONDILGH 349

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 Job time: 198 sec

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